```
RAW SEQUENCE LISTING                    DATE: 01/31/2001
PATENT APPLICATION:  US/09/510,332      TIME: 13:36:28

Input Set : A:\Uc-980-1.TXT
Output Set: N:\CRF3\01312001\I510332.raw
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 3 <110> APPLICANT: Zuker, Charles S.
 4        Adler, Jon Elliot
 5        Ryba, Nick
 6        Mueller, Ken
 7        Hoon, Mark
 8        The Regents of the University of California
10 <120> TITLE OF INVENTION: T2R, a Novel Family of Taste Receptors
12 <130> FILE REFERENCE: 02307E-098010US
14 <140> CURRENT APPLICATION NUMBER: US 09/510,332
15 <141> CURRENT FILING DATE: 2000-02-22
17 <150> PRIOR APPLICATION NUMBER: US 09/393,634
18 <151> PRIOR FILING DATE: 1999-09-10
20 <160> NUMBER OF SEQ ID NOS: 172
22 <170> SOFTWARE: PatentIn Ver. 2.1
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25 <211> LENGTH: 299
26 <212> TYPE: PRT
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <223> OTHER INFORMATION: human T2R01 (hGR01)
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34  1               5                   10                  15
36 Phe Leu Leu Gly Ile Phe Thr Asn Gly Ile Ile Val Val Val Asn Gly
37              20                  25                  30
39 Ile Asp Leu Ile Lys His Arg Lys Met Ala Pro Leu Asp Leu Leu Leu
40              35                  40                  45
42 Ser Cys Leu Ala Val Ser Arg Ile Phe Leu Gln Leu Phe Ile Phe Tyr
43      50                  55                  60
45 Val Asn Val Ile Val Ile Phe Phe Ile Glu Phe Ile Met Cys Ser Ala
46  65                  70                  75                  80
48 Asn Cys Ala Ile Leu Leu Phe Ile Asn Glu Leu Glu Leu Trp Leu Ala
49              85                  90                  95
51 Thr Trp Leu Gly Val Phe Tyr Cys Ala Lys Val Ala Ser Val Arg His
52              100                 105                 110
54 Pro Leu Phe Ile Trp Leu Lys Met Arg Ile Ser Lys Leu Val Pro Trp
55              115                 120                 125
57 Met Ile Leu Gly Ser Leu Leu Tyr Val Ser Met Ile Cys Val Phe His
58      130                 135                 140
60 Ser Lys Tyr Ala Gly Phe Met Val Pro Tyr Phe Leu Arg Lys Phe Phe
61 145                 150                 155                 160
63 Ser Gln Asn Ala Thr Ile Gln Lys Glu Asp Thr Leu Ala Ile Gln Ile
64              165                 170                 175
66 Phe Ser Phe Val Ala Glu Phe Ser Val Pro Leu Leu Ile Phe Leu Phe
67              180                 185                 190
69 Ala Val Leu Leu Leu Ile Phe Ser Leu Gly Arg His Thr Arg Gln Met
70              195                 200                 205
```

```
 72 Arg Asn Thr Val Ala Gly Ser Arg Val Pro Gly Arg Gly Ala Pro Ile
 73     210             215                 220
 75 Ser Ala Leu Leu Ser Ile Leu Ser Phe Leu Ile Leu Tyr Phe Ser His
 76 225             230                 235                 240
 78 Cys Met Ile Lys Val Phe Leu Ser Ser Leu Lys Phe His Ile Arg Arg
 79             245                 250                 255
 81 Phe Ile Phe Leu Phe Phe Ile Leu Val Ile Gly Ile Tyr Pro Ser Gly
 82             260                 265                 270
 84 His Ser Leu Ile Leu Ile Leu Gly Asn Pro Lys Leu Lys Gln Asn Ala
 85         275                 280                 285
 87 Lys Lys Phe Leu Leu His Ser Lys Cys Cys Gln
 88     290                 295
 91 <210> SEQ ID NO: 2
 92 <211> LENGTH: 900
 93 <212> TYPE: DNA
 94 <213> ORGANISM: Homo sapiens
 96 <220> FEATURE:
 97 <223> OTHER INFORMATION: human T2R01 (hGR01)
 99 <400> SEQUENCE: 2
100 atgctagagt ctcacctcat tatctatttt cttcttgcag tgatacaatt tcttcttggg 60
101 attttcacaa atggcatcat tgtggtggtg aatggcattg acttgatcaa gcacagaaaa 120
102 atggctccgc tggatctcct tctttcttgt ctggcagttt ctagaatttt tctgcagttg 180
103 ttcatcttct acgttaatgt gattgttatc ttcttcatag aattcatcat gtgttctgcg 240
104 aattgtgcaa ttctcttatt tataaatgaa ttggaacttt ggcttgccac atggctcggc 300
105 gttttctatt gtgccaaggt tgccagcgtc cgtcacccac tcttcatctg gttgaagatg 360
106 aggatatcca agctggtccc atggatgatc ctggggtctc tgctatatgt atctatgatt 420
107 tgtgtttttcc atagcaaata tgcagggttt atggtcccat acttcctaag gaaatttttc 480
108 tcccaaaatg ccacaattca aaaagaagat acactggcta tacagatttt ctcttttgtt 540
109 gctgagttct cagtgccatt gcttatcttc cttttttgctg ttttgctctt gatttttctct 600
110 ctggggaggc acaccgggca aatgagaaac acagtggccg gcagcagggt tcctggcagg 660
111 ggtgcaccca tcagcgcgtt gctgtctatc ctgtccttcc tgatcctcta cttctcccac 720
112 tgcatgataa aagtttttct ctcttctcta aagtttcaca tcagaaggtt catctttctg 780
113 ttcttcatcc ttgtgattgg tatataccct tctggacact ctctcatctt aattttagga 840
114 aatcctaaat tgaaacaaaa tgcaaaaaag ttcctcctcc acagtaagtg ctgtcagtga 900
117 <210> SEQ ID NO: 3
118 <211> LENGTH: 302
119 <212> TYPE: PRT
120 <213> ORGANISM: Homo sapiens
122 <220> FEATURE:
123 <223> OTHER INFORMATION: human T2R02 (hGR02)
125 <220> FEATURE:
126 <221> NAME/KEY: MOD_RES
127 <222> LOCATION: (143)
128 <223> OTHER INFORMATION: Xaa = any amino acid
130 <400> SEQUENCE: 3
131 Met Ala Leu Ser Phe Ser Ala Ile Leu His Ile Ile Met Met Ser Ala
132   1             5                 10                 15
134 Glu Phe Phe Thr Gly Ile Thr Val Asn Gly Phe Leu Ile Ile Val Asn
135             20                 25                 30
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137 Cys Asn Glu Leu Ile Lys His Arg Lys Leu Met Pro Ile Gln Ile Leu
138         35              40                  45
140 Leu Met Cys Ile Gly Met Ser Arg Phe Gly Leu Gln Met Val Leu Met
141     50              55              60
143 Val Gln Ser Phe Phe Ser Val Phe Phe Pro Leu Leu Tyr Val Lys Ile
144 65              70              75              80
146 Ile Tyr Gly Ala Ala Met Met Phe Leu Trp Met Phe Phe Ser Ser Ile
147             85              90                  95
149 Ser Leu Trp Phe Ala Thr Cys Leu Ser Val Phe Tyr Cys Leu Lys Ile
150             100             105             110
152 Ser Gly Phe Thr Gln Ser Cys Phe Leu Trp Leu Lys Phe Arg Ile Pro
153         115             120                 125         /
155 Lys Leu Ile Pro Trp Leu Phe Trp Glu Ala Phe Trp Pro Leu Xaa Ala
156     130             135             140
158 Leu His Leu Cys Val Glu Val Asp Tyr Ala Lys Asn Val Glu Glu Asp
159 145             150             155                 160
161 Ala Leu Arg Asn Thr Thr Leu Lys Lys Ser Lys Thr Lys Ile Lys Lys
162             165             170             175
164 Ile Ser Glu Val Leu Leu Val Asn Leu Ala Leu Ile Phe Pro Leu Ala
165             180             185             190
167 Ile Phe Val Met Cys Thr Ser Met Leu Leu Ile Ser Leu Tyr Lys His
168         195             200             205
170 Thr His Arg Met Gln His Gly Ser His Gly Phe Arg Asn Ala Asn Thr
171     210             215             220
173 Glu Ala His Ile Asn Ala Leu Lys Thr Val Ile Thr Phe Phe Cys Phe
174 225             230             235                 240
176 Phe Ile Ser Tyr Phe Ala Ala Phe Met Thr Asn Met Thr Phe Ser Leu
177             245             250             255
179 Pro Tyr Arg Ser His Gln Phe Phe Met Leu Lys Asp Ile Met Ala Ala
180             260             265             270
182 Tyr Pro Ser Gly His Ser Val Ile Ile Leu Ser Asn Ser Lys Phe
183     275             280             285
185 Gln Gln Ser Phe Arg Arg Ile Leu Cys Leu Lys Lys Lys Leu
186     290             295             300
189 <210> SEQ ID NO: 4
190 <211> LENGTH: 910
191 <212> TYPE: DNA
192 <213> ORGANISM: Homo sapiens
194 <220> FEATURE:
195 <223> OTHER INFORMATION: human T2R02 (hGR02)
197 <220> FEATURE:
198 <223> OTHER INFORMATION: human T2R02 (hGR02)
200 <400> SEQUENCE: 4
201 atggccttgt cttttcagc tattcttcat attatcatga tgtcagcaga attcttcaca 60
202 gggatcacag taaatggatt tcttatcatt gttaactgta atgaattgat caaacataga 120
203 aagctaatgc caattcaaat cctcttaatg tgcatagega tgtctagatt tggtctgcag 180
204 atggtgttaa tggtacaaag ttttttctct gtgttctttc cactcctta cgtcaaaata 240
205 atttatggtg cagcaatgat gttcctttgg atgtttttta gctctatcag cctatggttt 300
206 gccacttgcc tttctgtatt ttactgcctc aagatttcag gcttcactca gtcctgtttt 360
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207 ctttggttga aattcaggat cccaaagtta ataccttggc tgcttctggg aagcgttctg 420
208 gcctctgtga gcattgcatc tgtgtgtcga ggtagattac gctaaaaatg tggaagagga 480
209 tgccctcaga aacaccacac taaaaaagag taaaacaaag ataaagaaaa ttagtgaagt 540
210 gcttcttgtc aacttggcat taatatttcc tctagccata tttgtgatgt gcacttctat 600
211 gttactcatc tctctttaca agcacactca tcggatgcaa catggatctc atggctttag 660
212 aaatgccaac acagaagccc atataaatgc attaaaaaca gtgataacat tcttttgctt 720
213 ctttatttct tattttgctg ccttcatgac aaatatgaca tttagtttac cttacagaag 780
214 tcaccagttc tttatgctga aggacataat ggcagcatat ccctctggcc actcggttat 840
215 aataatcttg agtaattcta agttccaaca atcatttaga agaattctct gcctcaaaaa 900
216 gaaactatga                                                       910
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219 <210> SEQ ID NO: 5
220 <211> LENGTH: 316
221 <212> TYPE: PRT
222 <213> ORGANISM: Homo sapiens
224 <220> FEATURE:
225 <223> OTHER INFORMATION: human T2R03 (hGR03)
227 <400> SEQUENCE: 5
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228 Met Met Gly Leu Thr Glu Gly Val Phe Leu Ile Leu Ser Gly Thr Gln
229  1               5                  10                  15
231 Phe Thr Leu Gly Ile Leu Val Asn Cys Phe Ile Glu Leu Val Asn Gly
232              20                  25                  30
234 Ser Ser Trp Phe Lys Thr Lys Arg Met Ser Leu Ser Asp Phe Ile Ile
235          35                  40                  45
237 Thr Thr Leu Ala Leu Leu Arg Ile Ile Leu Leu Cys Ile Ile Leu Thr
238      50                  55                  60
240 Asp Ser Phe Leu Ile Glu Phe Ser Pro Asn Thr His Asp Ser Gly Ile
241  65                  70                  75                  80
243 Ile Met Gln Ile Ile Asp Val Ser Trp Thr Phe Thr Asn His Leu Ser
244                  85                  90                  95
246 Ile Trp Leu Ala Thr Cys Leu Gly Val Leu Tyr Cys Leu Lys Ile Ala
247              100                 105                 110
249 Ser Phe Ser His Pro Thr Phe Leu Trp Leu Lys Trp Arg Val Ser Arg
250          115                 120                 125
252 Val Met Val Trp Met Leu Leu Gly Ala Leu Leu Leu Ser Cys Gly Ser
253      130                 135                 140
255 Thr Ala Ser Leu Ile Asn Glu Phe Lys Leu Tyr Ser Val Phe Arg Gly
256 145                 150                 155                 160
258 Ile Glu Ala Thr Arg Asn Val Thr Glu His Phe Arg Lys Lys Arg Ser
259                  165                 170                 175
261 Glu Tyr Tyr Leu Ile His Val Leu Gly Thr Leu Trp Tyr Leu Pro Pro
262                  180                 185                 190
264 Leu Ile Val Ser Leu Ala Ser Tyr Ser Leu Leu Ile Phe Ser Leu Gly
265              195                 200                 205
267 Arg His Thr Arg Gln Met Leu Gln Asn Gly Thr Ser Ser Arg Asp Pro
268      210                 215                 220
270 Thr Thr Glu Ala His Lys Arg Ala Ile Arg Ile Ile Leu Ser Phe Phe
271 225                 230                 235                 240
273 Phe Leu Phe Leu Leu Tyr Phe Leu Ala Phe Leu Ile Ala Ser Phe Gly
274              245                 250                 255
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276 Asn Phe Leu Pro Lys Thr Lys Met Ala Lys Met Ile Gly Glu Val Met
277             260             265             270
279 Thr Met Phe Tyr Pro Ala Gly His Ser Phe Ile Leu Ile Leu Gly Asn
280         275             280             285
282 Ser Lys Leu Lys Gln Thr Phe Val Val Met Leu Arg Cys Glu Ser Gly
283         290             295             300
285 His Leu Lys Pro Gly Ser Lys Gly Pro Ile Phe Ser
286 305             310             315
289 <210> SEQ ID NO: 6
290 <211> LENGTH: 951
291 <212> TYPE: DNA
292 <213> ORGANISM: Homo sapiens
294 <220> FEATURE:
295 <223> OTHER INFORMATION: human T2R03 (hGR03)
297 <400> SEQUENCE: 6
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299 attctggtca attgtttcat tgagttggtc aatggtagca gctggttcaa gaccaagaga 120
300 atgtctttgt ctgacttcat catcaccacc ctggcactct tgaggatcat tctgctgtgt 180
301 attatcttga ctgatagttt tttaatagaa ttctctccca acacacatga ttcagggata 240
302 ataatgcaaa ttattgatgt ttcctggaca tttacaaacc atctgagcat ttggcttgcc 300
303 acctgtcttg gtgtcctcta ctgcctgaaa atcgccagtt tctctcaccc cacattcctc 360
304 tggctcaagt ggagagtttc tagggtgatg gtatggatgc tgttgggtgc actgctctta 420
305 tcctgtggta gtaccgcatc tctgatcaat gagtttaagc tctattctgt ctttagggga 480
306 attgaggcca ccaggaatgt gactgaacac ttcagaaaga agaggagtga gtattatctg 540
307 atccatgttc ttgggactct gtggtacctg cctcccttaa ttgtgtccct ggcctcctac 600
308 tctttgctca tcttctccct ggggaggcac acacggcaga tgctgcaaaa tgggacaagc 660
309 tccagagatc caaccactga ggcccacaag agggccatca gaatcatcct ttccttcttc 720
310 tttctcttct tacttactt tcttgctttc ttaattgcat catttggtaa tttcctacca 780
311 aaaaccaaga tggctaagat gattggcgaa gtaatgacaa tgttttatcc tgctggccac 840
312 tcatttattc tcattctggg gaacagtaag ctgaagcaga catttgtagt gatgctccgg 900
313 tgtgagtctg gtcatctgaa gcctggatcc aagggaccca ttttctctta g 951
316 <210> SEQ ID NO: 7
317 <211> LENGTH: 299
318 <212> TYPE: PRT
319 <213> ORGANISM: Homo sapiens
321 <220> FEATURE:
322 <223> OTHER INFORMATION: human T2R04 (hGR04)
324 <400> SEQUENCE: 7
325 Met Leu Arg Leu Phe Tyr Phe Ser Ala Ile Ile Ala Ser Val Ile Leu
326   1             5             10             15
328 Asn Phe Val Gly Ile Ile Met Asn Leu Phe Ile Thr Val Val Asn Cys
329             20             25             30
331 Lys Thr Trp Val Lys Ser His Arg Ile Ser Ser Ser Asp Arg Ile Leu
332         35             40             45
334 Phe Ser Leu Gly Ile Thr Arg Phe Leu Met Leu Gly Leu Phe Leu Val
335         50             55             60
337 Asn Thr Ile Tyr Phe Val Ser Ser Asn Thr Glu Arg Ser Val Tyr Leu
338 65             70             75             80
340 Ser Ala Phe Phe Val Leu Cys Phe Met Phe Leu Asp Ser Ser Ser Val
```

FYI:

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Input Set : A:\Uc-980-1.TXT
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L:525  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:528  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:531  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:534  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:537  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:540  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:543  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:546  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:549  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:555  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:558  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:561  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:567  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
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L:1013 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1016 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1028 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1037 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1064 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1067 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1070 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1073 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1091 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1405 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:1558 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:1585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:1645 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:1782 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:1824 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:1850 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:1853 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:1856 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:1859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:1862 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:1865 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:1895 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:1928 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:1937 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:1955 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1956 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1957 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1958 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1959 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1961 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1963 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
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L:1965 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1985 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42